

SEQUENCE LISTING

<110> Reed, John C.
Pio, Frederick F.
Godzik, Adam
Stehlik, Christian
Damiano, Jason S.
Lee, Sug-Hyung
Oliveira, Vasco A.
Hayashi, Hideki
Pawlowski, Krzysztof

<120> Novel Card Domain Containing
Polypeptides, Encoding Nucleic Acids, and Methods of Use

<130> P-LJ 4752

<150> US 09/579,240
<151> 2000-05-24

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Lys Leu Leu Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr
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tta act tct cgg agg ctg att tct gag gaa gag tat gag act ctg gag 144
Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Tyr Glu Thr Leu Glu
35 40 45

aat gtt aca gat ctc ctg aag aaa agt cgg aag ctg tta att ttg gta 192
Asn Val Thr Asp Leu Leu Lys Ser Arg Lys Leu Leu Ile Leu Val

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Gln	Lys	Lys	Gly	Glu	Ala	Thr	Cys	Gln	His	Phe	Leu	Lys	Cys	Leu	Phe	
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agt	act	ttt	cca	cag	tca	gct	gcc	att	tgc	ggc	tta	agg	cat	gaa	gtt	288
Ser	Thr	Phe	Pro	Gln	Ser	Ala	Ala	Ile	Cys	Gly	Leu	Arg	His	Glu	Val	
85								90				95				
tta	aaa	cat	gag	aat	aca	gta	cct	cct	caa	tct	atg	ggg	gca	agc	agt	336
Leu	Lys	His	Glu	Asn	Thr	Val	Pro	Pro	Gln	Ser	Met	Gly	Ala	Ser	Ser	
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aat	tca	gaa	gat	gct	ttt	tct	cct	gga	ata	aaa	cag	cct	gaa	gcc	cct	384
Asn	Ser	Glu	Asp	Ala	Phe	Ser	Pro	Gly	Ile	Lys	Gln	Pro	Glu	Ala	Pro	
115								120				125				
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Glu	Ile	Thr	Val	Phe	Phe	Ser	Glu	Lys	Glu	His	Leu	Asp	Leu	Glu	Thr	
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Ser	Glu	Phe	Phe	Arg	Asp	Lys	Lys	Thr	Ser	Tyr	Arg	Glu	Thr	Ala	Leu	
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Ser	Ala	Arg	Lys	Asn	Glu	Lys	Glu	Tyr	Asp	Thr	Pro	Glu	Val	Thr	Leu	
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Ser	Tyr	Ser	Val	Glu	Lys	Val	Gly	Cys	Glu	Val	Pro	Ala	Thr	Ile	Thr	
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tat	ata	aaa	gat	gga	cag	aga	tat	gag	gag	cta	gat	gat	tct	tta	tac	624
Tyr	Ile	Lys	Asp	Gly	Gln	Arg	Tyr	Glu	Glu	Leu	Asp	Asp	Ser	Leu	Tyr	
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Leu	Gly	Lys	Glu	Glu	Tyr	Leu	Gly	Ser	Val	Asp	Thr	Pro	Glu	Asp	Ala	
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Glu	Ala	Thr	Val	Glu	Glu	Glu	Val	Tyr	Asp	Asp	Pro	Glu	His	Val	Gly	
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Tyr	Asp	Gly	Glu	Glu	Asp	Phe	Glu	Asn	Ser	Glu	Thr	Thr	Glu	Phe	Ser	
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Gly	Glu	Glu	Pro	Ser	Tyr	Glu	Gly	Ser	Glu	Thr	Ser	Leu	Ser	Leu	Glu	
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Glu Glu Gln Glu Lys Ser Ile Glu Gly Trp Ser Arg Thr His Gly Leu
275 280 285

aag cga tcc tcc cac gtt ggc ctc cca aag tgc tgg gat tac agg cgt 912
Lys Arg Ser Ser His Val Gly Leu Pro Lys Cys Trp Asp Tyr Arg Arg
290 295 300

gag cca ccc tgc ctg gcc tgaaaattct gcctcaaaca tctcaaacat 960
Glu Pro Pro Cys Leu Ala
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aaaaaaaaaa aatctaga 1038

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<213> Homo sapien

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Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu
35 40 45
Asn Val Thr Asp Leu Leu Lys Ser Arg Lys Leu Leu Ile Leu Val
50 55 60
Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe
65 70 75 80
Ser Thr Phe Pro Gln Ser Ala Ala Ile Cys Gly Leu Arg His Glu Val
85 90 95
Leu Lys His Glu Asn Thr Val Pro Pro Gln Ser Met Gly Ala Ser Ser
100 105 110
Asn Ser Glu Asp Ala Phe Ser Pro Gly Ile Lys Gln Pro Glu Ala Pro
115 120 125
Glu Ile Thr Val Phe Phe Ser Glu Lys Glu His Leu Asp Leu Glu Thr
130 135 140
Ser Glu Phe Phe Arg Asp Lys Lys Thr Ser Tyr Arg Glu Thr Ala Leu
145 150 155 160
Ser Ala Arg Lys Asn Glu Lys Glu Tyr Asp Thr Pro Glu Val Thr Leu
165 170 175
Ser Tyr Ser Val Glu Lys Val Gly Cys Glu Val Pro Ala Thr Ile Thr
180 185 190
Tyr Ile Lys Asp Gly Gln Arg Tyr Glu Glu Leu Asp Asp Ser Leu Tyr
195 200 205
Leu Gly Lys Glu Glu Tyr Leu Gly Ser Val Asp Thr Pro Glu Asp Ala
210 215 220
Glu Ala Thr Val Glu Glu Val Tyr Asp Asp Pro Glu His Val Gly
225 230 235 240
Tyr Asp Gly Glu Glu Asp Phe Glu Asn Ser Glu Thr Thr Glu Phe Ser

245	250	255
Gly Glu Glu Pro Ser Tyr Glu Gly Ser Glu Thr Ser Leu Ser Leu Glu		
260	265	270
Glu Glu Gln Glu Lys Ser Ile Glu Gly Trp Ser Arg Thr His Gly Leu		
275	280	285
Lys Arg Ser Ser His Val Gly Leu Pro Lys Cys Trp Asp Tyr Arg Arg		
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Glu Pro Pro Cys Leu Ala		
305	310	

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gtc gag ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg 96
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu
20 25 30

gac tgg ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc 144
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
35 40 45

ttc cac ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg 192
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu
50 55 60

gac acc gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc atc gcg Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala 65 70 75 80	240
gct gcc caa gaa gcc cag gcc gac agc cag tcc ccc aag ctg cat ggc Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly 85 90 95	288
tgc tgg gac ccc cac tcg ctc cac cca gcc cga gac ctg cag agt cac Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His 100 105 110	336
cg ^g cca gcc att gtc agg agg ctc cac agc cat gtg gag aac atg ctg Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu 115 120 125	384
gac ctg gca tgg gag cg ^g ggt ttc gtc agc cag tat gaa tgt gat gaa Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu 130 135 140	432
atc agg ttg cc ^g atc ttc aca cc ^g tcc cag agg gca aga agg ctg ctt Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu 145 150 155 160	480
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cat gtt cag gaa tta cca gtc cca ttg gcc ctg cct ttg gaa gct gcc His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala 180 185 190	576
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tct cgc ttc ctc agt acc tat gat gga gca gag acg ctc tgc ctg gag Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu 210 215 220	672
gac ata tac aca gag aat gtc ctg gag gtc tgg gca gat gtg ggc atg Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met 225 230 235 240	720
gct gga ccc cc ^g cag aag agc cca gcc acc ctg ggc ctg gag gag ctc Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu 245 250 255	768
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gtg ggt gag ggc agt ggc aag agc acg ctc ctg cag cg ^g ctg cac	864

Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His
275 280 285

ttg ctg tgg gct gca ggg caa gac ttc cag gaa ttt ctc ttt gtc ttc 912
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe
290 295 300

cca ttc agc tgc cgg cag ctg cag tgc atg gcc aaa cca ctc tct gtg 960
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val
305 310 315 320

cgg act cta ctc ttt gag cac tgc tgt tgg cct gat gtt ggt caa gaa 1008
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu
325 330 335

gac atc ttc cag tta ctc ctt gac cac cct gac cgt gtc ctg tta acc 1056
Asp Ile Phe Gln Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr
340 345 350

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Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg
355 360 365

cac tgc tcc ccg acc gac ccc acc tct gtc cag acc ctg ctc ttc aac 1152
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn
370 375 380

ctt ctg cag ggc aac ctg ctg aag aat gcc cgc aag gtg gtg acc agc 1200
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser
385 390 395 400

cgt ccg gcc gct gtg tcg cgc ttc ctc agg aag tac atc cgc acc gag 1248
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu
405 410 415

ttc aac ctc aag ggc ttc tct gaa cag ggc atc gag ctg tac ctg agg 1296
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg
420 425 430

aag cgc cat cat gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc 1344
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu
435 440 445

caa gag acc tca gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca 1392
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser
450 455 460

tgg atg gtg tcc aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg 1440
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly
465 470 475 480

tcc cca aag acc act aca gat atg tac ctg ctg att ctg cag cat ttt 1488
Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe

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490

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ctg ctg cat gcc acc ccc cca gac tca gct tcc caa ggt ctg gga ccc 1536
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
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agt ctt ctt cgg ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg 1584
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Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
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Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
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<211> 560

<212> PRT

<213> Homo sapien

<400> 83

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20 25 30
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly

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Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu		
50	55	60
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala		
65	70	75
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly		
85	90	95
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His		
100	105	110
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu		
115	120	125
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu		
130	135	140
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu		
145	150	155
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln		
165	170	175
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala		
180	185	190
Thr Cys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln		
195	200	205
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu		
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Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met		
225	230	235
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu		
245	250	255
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val		
260	265	270
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His		
275	280	285
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe		
290	295	300
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val		
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Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu		
325	330	335
Asp Ile Phe Gln Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr		
340	345	350
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg		
355	360	365
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn		
370	375	380
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser		
385	390	395
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu		
405	410	415
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg		
420	425	430
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu		
435	440	445
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser		
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Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly
465 470 475 480
Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe
485 490 495
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
500 505 510
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
515 520 525
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
530 535 540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545 550 555 560

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<213> Homo sapien

<400> 84
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aaaaagtgc ttgaaatcct tcaacatgtat cctgattcta tcttagacac gttaacttct 180
cgaggcgtga tttctgagga agagttatgag actctggaga atgttacaga tctcctgaaag 240
aaaagtcgga agctgttaat tttggtacag aaaaagggag aggccacctg tcagcatttt 300
ctcaagtgtt tatttagtac ttttccacag tcagctgcca tttgcggctt aaggcatgaa 360
gtttaaaac atgagaatac agtacccctt caatctatgg gggcaagcag taattcagaa 420
gatgttttt ctcctggaat aaaacagcct gaagccctg agatcacagt gttcttcagt 480
gagaaggaac acttggattt ggaaacctct gagttttca gggacaagaa aacttagttat 540
agggaaaacag ctttgtctgc caggaagaat gagaaggaaat atgacacacc agaagtccaca 600
ttatcatatt cagttgagaa agttggatgt gaagttccag caactattac atatataaaa 660
gatggacaga gatatgagga gctagatgtat tctttataact taggaaaaga ggaatatctt 720
ggatctgttg acaccctgta agatgcagaa gccactgtgg aagaggaggt ttatgtatgac 780
ccagagcacg ttggatatga tggtaagag gacttcgaga attcagaaac cacagagttc 840
tctggatggaa aaccaagtta tgagggatca gaaaccagcc tttcattgga ggaggaacag 900
gagaaaaagta tagaaggctg gtctcgaact catgggctta agcgatcctc ccacgttggc 960
ctcccaaagt gctgggatca caggcgtgag ccaccctgccc tggcctgaaa attctgcctc 1020
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<210> 85
<211> 510
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (15) ... (305)

<400> 85
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1 5 10

ttt atc cat tcc atg ggt gaa ggt aca ata aat ggc tta ctg gat gaa	98
Phe Ile His Ser Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu	
15 20 25	
tta tta cag aca agg gtg ctg aac cag gaa gag atg gag aaa gta aaa	146
Leu Leu Gln Thr Arg Val Leu Asn Gln Glu Glu Met Glu Lys Val Lys	
30 35 40	
cgt gaa aat gct aca gtt atg gat aag acc cga gct ttg att gac tcc	194
Arg Glu Asn Ala Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser	
45 50 55 60	
gtt att ccg aaa ggg gca cag gca tgc caa att tgc atc aca tac att	242
Val Ile Pro Lys Gly Ala Gln Ala Cys Gln Ile Cys Thr Tyr Ile	
65 70 75	
tgt gaa gaa gac agt tac ctg gca gag acg ctg gga ctc tca gca ggt	290
Cys Glu Glu Asp Ser Tyr Leu Ala Glu Thr Leu Gly Leu Ser Ala Gly	
80 85 90	
ccg ata cct gga aat tagcttagct tagtacacaa gactccaaat tactatttc	345
Pro Ile Pro Gly Asn	
95	
ttccttccca gctttcagg cagtgcagga caacccagct atgcccacat gctcaagccc	405
agaaggcaga atcaagctt gcttctaga agacgctcaa aggatatgga aacaaaagtt	465
gcagagggtgc catgttcaga atacaataat aaagtggagt aaaga	510
<210> 86	
<211> 97	
<212> PRT	
<213> Homo sapien	
<400> 86	
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1 5 10 15	
Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr	
20 25 30	
Arg Val Leu Asn Gln Glu Met Glu Lys Val Lys Arg Glu Asn Ala	
35 40 45	
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys	
50 55 60	
Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp	
65 70 75 80	
Ser Tyr Leu Ala Glu Thr Leu Gly Leu Ser Ala Gly Pro Ile Pro Gly	
85 90 95	
Asn	

<210> 87
<211> 97

<212> PRT

<213> Homo sapien

<400> 87

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20 25 30
Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala
35 40 45
Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys
50 55 60
Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp
65 70 75 80
Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly
85 90 95
Asn

<210> 88

<400> 88
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<210> 89

<211> 321

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(318)

<400> 89

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Met Ile Leu Leu Lys Lys Arg Arg Leu Leu Ile Asn Ser Leu Gly Glu
1 5 10 15

ggt aca ata aat ggc tta ctg gat gaa tta ttg gag aca aat gtg ctg 96
Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Thr Asn Val Leu
20 25 30

agc cag gaa gac aca gag ata gta aaa tgt gaa aat gtt aca gtt atc 144
Ser Gln Glu Asp Thr Glu Ile Val Lys Cys Glu Asn Val Thr Val Ile
35 40 45

gat aag gcc cga gat ttg ctt gac tct gtt att cgg aaa ggg gca ggg 192
Asp Lys Ala Arg Asp Leu Leu Asp Ser Val Ile Arg Lys Gly Ala Gly
50 55 60

gca tgt gaa att tgc atc aca tac att tgt gaa gaa gac agg tac ctg 240
Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Arg Tyr Leu

65	70	75	80	
gca ggg acg ctg gga ctc tca gca gga aat gac tac aga gct gga ggc				288
Ala Gly Thr Leu Gly Leu Ser Ala Gly Asn Asp Tyr Arg Ala Gly Gly				
85	90	95		

att tgc tca ccg ccc aga gca caa gac ctc tga				321
Ile Cys Ser Pro Pro Arg Ala Gln Asp Leu				
100	105			

<210> 90
<211> 106
<212> PRT
<213> Homo sapien

<400> 90

Met Ile Leu Leu Lys Lys Arg Arg Leu Leu Ile Asn Ser Leu Gly Glu				
1	5	10	15	
Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Thr Asn Val Leu				
20	25	30		
Ser Gln Glu Asp Thr Glu Ile Val Lys Cys Glu Asn Val Thr Val Ile				
35	40	45		
Asp Lys Ala Arg Asp Leu Leu Asp Ser Val Ile Arg Lys Gly Ala Gly				
50	55	60		
Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Arg Tyr Leu				
65	70	75	80	
Ala Gly Thr Leu Gly Leu Ser Ala Gly Asn Asp Tyr Arg Ala Gly Gly				
85	90	95		
Ile Cys Ser Pro Pro Arg Ala Gln Asp Leu				
100	105			

<210> 91
<211> 108
<212> PRT
<213> Homo sapien

<400> 91

Met Ala Asp Lys Val Leu Leu Glu Lys Arg Lys Leu Leu Ile Asn Ser				
1	5	10	15	
Leu Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Glu Thr				
20	25	30		
Asn Val Leu Ser Gln Glu Asp Glu Ile Val Lys Arg Glu Asn Ala Thr				
35	40	45		
Val Ile Asp Lys Ala Arg Ala Leu Leu Asp Ser Val Ile Arg Lys Gly				
50	55	60		
Ala Gly Ala Cys Glu Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp Ser				
65	70	75	80	
Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Gly Asn Ala Val Gln Ala				
85	90	95		
Gly Gly Ala Cys Ser Thr Ser Ser Gly Gln Asp Leu				
100	105			

<210> 92

<400> 92
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<210> 93

<400> 93
000

<210> 94

<400> 94
000

<210> 95

<400> 95
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<210> 96

<211> 3396

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (277) ... (3348)

<400> 96

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acatctgctg gaagtccctc gggattcaag gtacaggaa tgaagagtag ttttacagaa 180
aaaagaggac aatattggga tcaccttga cctttccatt tgaaaataat attttctatt 240
gtgttataga aaggtggaa gctttcatcc agaaca atg aat ttc ata aag gac 294

Met Asn Phe Ile Lys Asp

1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486

Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu			
55	60	65	70
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga			534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly			
75	80	85	
caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct			582
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala			
90	95	100	
cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat			630
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr			
105	110	115	
ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc			678
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe			
120	125	130	
aca gaa cct atc ctg tgg agg aag gac caa cac cat cac cgc gtg gag			726
Thr Glu Pro Ile Leu Trp Arg Lys Asp Gln His His Arg Val Glu			
135	140	145	150
cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc			774
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile			
155	160	165	
att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att			822
Ile Glu Gly Glu Ser Gly Lys Ser Thr Leu Leu Gln Arg Ile			
170	175	180	
gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa			870
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys			
185	190	195	
tcc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa			918
Phe Val Phe Leu Arg Leu Ser Arg Ala Gln Gly Leu Phe Glu			
200	205	210	
acc ctc tgt gat caa ctc ctg gat ata cct ggc aca atc agg aag cag			966
Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro Gly Thr Ile Arg Lys Gln			
215	220	225	230
aca ttc atg gcc atg ctg ctg aag ctg cgg cag agg gtt ctt ttc ctt			1014
Thr Phe Met Ala Met Leu Leu Lys Leu Arg Gln Arg Val Leu Phe Leu			
235	240	245	
ctt gat ggc tac aat gaa ttc aag ccc cag aac tgc cca gaa atc gaa			1062
Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln Asn Cys Pro Glu Ile Glu			
250	255	260	
gcc ctg ata aag gaa aac cac cgc ttc aag aac atg gtc atc gtc acc			1110
Ala Leu Ile Lys Glu Asn His Arg Phe Lys Asn Met Val Ile Val Thr			

265	270	275	
act acc act gag tgc ctg agg cac ata cgg cag ttt ggt gcc ctg act			1158
Thr Thr Thr Glu Cys Leu Arg His Ile Arg Gln Phe Gly Ala Leu Thr			
280	285	290	
gct gag gtg ggg gat atg aca gaa gac agc gcc cag gct ctc atc cga			1206
Ala Glu Val Gly Asp Met Thr Glu Asp Ser Ala Gln Ala Leu Ile Arg			
295	300	305	310
gaa gtg ctg atc aag gag ctt gct gaa ggc ttg ttg ctc caa att cag			1254
Glu Val Leu Ile Lys Glu Leu Ala Glu Gly Leu Leu Leu Gln Ile Gln			
315	320	325	
aaa tcc agg tgc ttg agg aat ctc atg aag acc cct ctc ttt gtg gtc			1302
Lys Ser Arg Cys Leu Arg Asn Leu Met Lys Thr Pro Leu Phe Val Val			
330	335	340	
atc act tgt gca atc cag atg ggt gaa agt gag ttc cac tct cac aca			1350
Ile Thr Cys Ala Ile Gln Met Gly Glu Ser Glu Phe His Ser His Thr			
345	350	355	
caa aca acg ctg ttc cat acc ttc tat gat ctg ttg ata cag aaa aac			1398
Gln Thr Thr Leu Phe His Thr Phe Tyr Asp Leu Leu Ile Gln Lys Asn			
360	365	370	
aaa cac aaa cat aaa ggt gtg gct gca agt gac ttc att cgg agc ctg			1446
Lys His Lys His Gly Val Ala Ala Ser Asp Phe Ile Arg Ser Leu			
375	380	385	390
gac cac cgt gga gac cta gct ctg gag ggt gtg ttc tcc cac aag ttt			1494
Asp His Arg Gly Asp Leu Ala Leu Glu Gly Val Phe Ser His Lys Phe			
395	400	405	
gat ttc gaa ctg cag gat gtg tcc agc gtg aat gag gat gtc ctg ctg			1542
Asp Phe Glu Leu Gln Asp Val Ser Ser Val Asn Glu Asp Val Leu Leu			
410	415	420	
aca act ggg ctc ctc tgt aaa tat aca gct caa agg ttc aag cca aag			1590
Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala Gln Arg Phe Lys Pro Lys			
425	430	435	
tat aaa ttc ttt cac aag tca ttc cag gag tac aca gca gga cga aga			1638
Tyr Lys Phe Phe His Lys Ser Phe Gln Glu Tyr Thr Ala Gly Arg Arg			
440	445	450	
ctc agc agt tta ttg acg tct cat gag cca gag gag gtg acc aag ggg			1686
Leu Ser Ser Leu Leu Thr Ser His Glu Pro Glu Glu Val Thr Lys Gly			
455	460	465	470
aat ggt tac ttg cag aaa atg gtt tcc att tcg gac att aca tcc act			1734
Asn Gly Tyr Leu Gln Lys Met Val Ser Ile Ser Asp Ile Thr Ser Thr			
475	480	485	

tat agc agc ctg ctc cg ^g tac acc tgt ggg tca tct gtg gaa gcc acc		1782
Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly Ser Ser Val Glu Ala Thr		
490	495	500
agg gct gtt atg aag cac ctc gca gca gtg tat caa cac ggc tgc ctt		1830
Arg Ala Val Met Lys His Leu Ala Ala Val Tyr Gln His Gly Cys Leu		
505	510	515
ctc gga ctt tcc atc gcc aag agg cct ctc tgg aga cag gaa tct ttg		1878
Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu Trp Arg Gln Glu Ser Leu		
520	525	530
caa agt gtg aaa aac acc act gag caa gaa att ctg aaa gcc ata aac		1926
Gln Ser Val Lys Asn Thr Thr Glu Gln Glu Ile Leu Lys Ala Ile Asn		
535	540	545
550		
atc aat tcc ttt gta gag tgt ggc atc cat tta tat caa gag agt aca		1974
Ile Asn Ser Phe Val Glu Cys Gly Ile His Leu Tyr Gln Glu Ser Thr		
555	560	565
tcc aaa tca gcc ctg agc caa gaa ttt gaa gct ttc ttt caa ggt aaa		2022
Ser Lys Ser Ala Leu Ser Gln Glu Phe Glu Ala Phe Phe Gln Gly Lys		
570	575	580
agc tta tat atc aac tca ggg aac atc ccc gat tac tta ttt gac ttc		2070
Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro Asp Tyr Leu Phe Asp Phe		
585	590	595
ttt gaa cat ttg ccc aat tgt gca agt gcc ctg gac ttc att aaa ctg		2118
Phe Glu His Leu Pro Asn Cys Ala Ser Ala Leu Asp Phe Ile Lys Leu		
600	605	610
gac ttt tat ggg gga gct atg gct tca tgg gaa aag gct gca gaa gac		2166
Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp Glu Lys Ala Ala Glu Asp		
615	620	625
630		
aca ggt gga atc cac atg gaa gag gcc cca gaa acc tac att ccc agc		2214
Thr Gly Gly Ile His Met Glu Glu Ala Pro Glu Thr Tyr Ile Pro Ser		
635	640	645
agg gct gta tct ttg ttc aac tgg aag cag gaa ttc agg act ctg		2262
Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln Glu Phe Arg Thr Leu		
650	655	660
gag gtc aca ctc cg ^g gat ttc agc aag ttg aat aag caa gat atc aga		2310
Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln Asp Ile Arg		
665	670	675
tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg ctg caa ata		2358
Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser Leu Arg Leu Gln Ile		
680	685	690

aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc ctc agc acc Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val Leu Ser Thr 695 700 705 710	2406
tgt aag aac att tat tct ctc atg gtg gaa gcc agt ccc ctc acc ata Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile 715 720 725	2454
gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser 730 735 740	2502
att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg act gac agc Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu Thr Asp Ser 745 750 755	2550
ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys 760 765 770	2598
atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu 775 780 785 790	2646
aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu 795 800 805	2694
gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu 810 815 820	2742
gaa gaa att caa tta gtc tcc tgc ttg tct gca aat gca gtg aaa Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys 825 830 835	2790
atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp 840 845 850	2838
tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu 855 860 865 870	2886
ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu 875 880 885	2934
ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His 890 895 900	2982
ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga	3030

Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg
905 910 915

ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac 3078
Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn
920 925 930

cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc 3126
Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser
935 940 945 950

agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa 3174
Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln
955 960 965

tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca 3222
Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala
970 975 980

tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa 3270
Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln
985 990 995

gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt 3318
Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val
1000 1005 1010

att aca ggt gct ttt aaa cta gta act gct taaataaaagt gtactcgaag 3368
Ile Thr Gly Ala Phe Lys Leu Val Thr Ala
1015 1020

ccaaaaaaaaaaaaaaaaaaaa 3396

<210> 97
<211> 1024
<212> PRT
<213> Homo sapien

<400> 97
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
20 25 30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly
85 90 95
Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro
100 105 110

Ser Phe Leu Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe
115 120 125
Asn Leu Lys Ser Thr Phe Thr Glu Pro Ile Leu Trp Arg Lys Asp Gln
130 135 140
His His His Arg Val Glu Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala
145 150 155 160
Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser
165 170 175
Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys
180 185 190
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala
195 200 205
Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
210 215 220
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
225 230 235 240
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
245 250 255
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys
260 265 270
Asn Met Val Ile Val Thr Thr Thr Glu Cys Leu Arg His Ile Arg
275 280 285
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
290 295 300
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
305 310 315 320
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
325 330 335
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
340 345 350
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
355 360 365
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
370 375 380
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
385 390 395 400
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
405 410 415
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
420 425 430
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
435 440 445
Tyr Thr Ala Gly Arg Arg Leu Ser Ser Leu Leu Thr Ser His Glu Pro
450 455 460
Glu Glu Val Thr Lys Gly Asn Gly Tyr Leu Gln Lys Met Val Ser Ile
465 470 475 480
Ser Asp Ile Thr Ser Thr Tyr Ser Ser Leu Leu Arg Tyr Thr Cys Gly
485 490 495
Ser Ser Val Glu Ala Thr Arg Ala Val Met Lys His Leu Ala Ala Val
500 505 510
Tyr Gln His Gly Cys Leu Leu Gly Leu Ser Ile Ala Lys Arg Pro Leu
515 520 525
Trp Arg Gln Glu Ser Leu Gln Ser Val Lys Asn Thr Thr Glu Gln Glu

530 535 540
Ile Leu Lys Ala Ile Asn Ile Asn Ser Phe Val Glu Cys Gly Ile His
545 550 555 560
Leu Tyr Gln Glu Ser Thr Ser Lys Ser Ala Leu Ser Gln Glu Phe Glu
565 570 575
Ala Phe Phe Gln Gly Lys Ser Leu Tyr Ile Asn Ser Gly Asn Ile Pro
580 585 590
Asp Tyr Leu Phe Asp Phe Glu His Leu Pro Asn Cys Ala Ser Ala
595 600 605
Leu Asp Phe Ile Lys Leu Asp Phe Tyr Gly Gly Ala Met Ala Ser Trp
610 615 620
Glu Lys Ala Ala Glu Asp Thr Gly Gly Ile His Met Glu Glu Ala Pro
625 630 635 640
Glu Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys
645 650 655
Gln Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu
660 665 670
Asn Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr
675 680 685
Ser Leu Arg Leu Gln Ile Lys Arg Cys Ala Gly Val Ala Gly Ser Leu
690 695 700
Ser Leu Val Leu Ser Thr Cys Lys Asn Ile Tyr Ser Leu Met Val Glu
705 710 715 720
Ala Ser Pro Leu Thr Ile Glu Asp Glu Arg His Ile Thr Ser Val Thr
725 730 735
Asn Leu Lys Thr Leu Ser Ile His Asp Leu Gln Asn Gln Arg Leu Pro
740 745 750
Gly Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu
755 760 765
Ile Met Asp Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys Leu Ala
770 775 780
Glu Gly Leu Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu Thr His
785 790 795 800
Leu Ser Asp Ile Gly Glu Gly Met Asp Tyr Ile Val Lys Ser Leu Ser
805 810 815
Ser Glu Pro Cys Asp Leu Glu Glu Ile Gln Leu Val Ser Cys Cys Leu
820 825 830
Ser Ala Asn Ala Val Lys Ile Leu Ala Gln Asn Leu His Asn Leu Val
835 840 845
Lys Leu Ser Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly
850 855 860
Asn Glu Ala Leu His Glu Leu Ile Asp Arg Met Asn Val Leu Glu Gln
865 870 875 880
Leu Thr Ala Leu Met Leu Pro Trp Gly Cys Asp Val Gln Gly Ser Leu
885 890 895
Ser Ser Leu Leu Lys His Leu Glu Glu Val Pro Gln Leu Val Lys Leu
900 905 910
Gly Leu Lys Asn Trp Arg Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly
915 920 925
Ala Phe Phe Gly Lys Asn Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu
930 935 940
Ala Gly Asn Arg Val Ser Ser Asp Gly Trp Leu Ala Phe Met Gly Val
945 950 955 960

Phe Glu Asn Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr Lys Glu
965 970 975
Phe Leu Pro Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val Leu Ser
980 985 990
Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe Asp
995 1000 1005
Asp Asp Asp Leu Ser Val Ile Thr Gly Ala Phe Lys Leu Val Thr Ala
1010 1015 1020

<210> 98
<211> 1395
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (277)...(1353)

<400> 98
cgcccgggca ggtgtttata ctccggagggtgtcccggtcgatcggtggagtggacc 60
aaaactggtgatctgtttgc cctgtgtgac cttgcccaga accctgctga ctgagagaac 120
acatctgctg gaagtcctct gggattcaag gtacaggaa tgaagagtagttttacagaa 180
aaaagaggac aatattggatcacccttgc cctttccatt tggaaataat attttctatt 240
gtgttataga aagggtggaa gcttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

caa agt ggt ctg act gac agc ttg ggt aac ttg aag aac ctt aca aag 582
Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn Leu Lys Asn Leu Thr Lys
90 95 100

ctc ata atg gat aac ata aag atg aat gaa gaa gat gct ata aaa cta 630

Leu Ile Met Asp Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys Leu
105 110 115

gct gaa ggc ctg aaa aac ctg aag aag atg tgt tta ttt cat ttg acc 678
Ala Glu Gly Leu Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu Thr
120 125 130

cac ttg tct gac att gga gag gga atg gat tac ata gtc aag tct ctg 726
His Leu Ser Asp Ile Gly Glu Gly Met Asp Tyr Ile Val Lys Ser Leu
135 140 145 150

tca agt gaa ccc tgt gac ctt gaa gaa att caa tta gtc tcc tgc tgc 774
Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile Gln Leu Val Ser Cys Cys
155 160 165

ttg tct gca aat gca gtg aaa atc cta gct cag aat ctt cac aat ttg 822
Leu Ser Ala Asn Ala Val Lys Ile Leu Ala Gln Asn Leu His Asn Leu
170 175 180

gtc aaa ctg agc att ctt gat tta tca gaa aat tac ctg gaa aaa gat 870
Val Lys Leu Ser Ile Leu Asp Leu Ser Glu Asn Tyr Leu Glu Lys Asp
185 190 195

gga aat gaa gct ctt cat gaa ctg atc gac agg atg aac gtg cta gaa 918
Gly Asn Glu Ala Leu His Glu Leu Ile Asp Arg Met Asn Val Leu Glu
200 205 210

cag ctc acc gca ctg atg ctg ccc tgg ggc tgt gac gtg caa ggc agc 966
Gln Leu Thr Ala Leu Met Leu Pro Trp Gly Cys Asp Val Gln Gly Ser
215 220 225 230

ctg agc agc ctg ttg aaa cat ttg gag gag gtc cca caa ctc gtc aag 1014
Leu Ser Ser Leu Leu Lys His Leu Glu Glu Val Pro Gln Leu Val Lys
235 240 245

ctt ggg ttg aaa aac tgg aga ctc aca gat aca gag att aga att tta 1062
Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp Thr Glu Ile Arg Ile Leu
250 255 260

ggt gca ttt ttt gga aag aac cct ctg aaa aac ttc cag cag ttg aat 1110
Gly Ala Phe Phe Gly Lys Asn Pro Leu Lys Asn Phe Gln Gln Leu Asn
265 270 275

ttg gcg gga aat cgt gtg agc agt gat gga tgg ctt gcc ttc atg ggt 1158
Leu Ala Gly Asn Arg Val Ser Ser Asp Gly Trp Leu Ala Phe Met Gly
280 285 290

gta ttt gag aat ctt aag caa tta gtg ttt ttt gac ttt agt act aaa 1206
Val Phe Glu Asn Leu Lys Gln Leu Val Phe Phe Asp Phe Ser Thr Lys
295 300 305 310

gaa ttt cta cct gat cca gca tta gtc aga aaa ctt agc caa gtg tta 1254
Glu Phe Leu Pro Asp Pro Ala Leu Val Arg Lys Leu Ser Gln Val Leu

315

320

325

tcc aag tta act ttt ctg caa gaa gct agg ctt gtt ggg tgg caa ttt 1302
Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg Leu Val Gly Trp Gln Phe
330 335 340

gat gat gat gat ctc agt gtt att aca ggt gct ttt aaa cta gta act 1350
Asp Asp Asp Asp Leu Ser Val Ile Thr Gly Ala Phe Lys Leu Val Thr
345 350 355

gct taaataaaagt gtactcgaag caaaaaaaaaa aaaaaaaaaa aa 1395
Ala

<210> 99
<211> 359
<212> PRT
<213> Homo sapien

<400> 99
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
20 25 30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Gly Leu Thr Asp Ser Leu Gly Asn
85 90 95
Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met Asn Glu
100 105 110
Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys Lys Met
115 120 125
Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly Met Asp
130 135 140
Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile
145 150 155 160
Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile Leu Ala
165 170 175
Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu Ser Glu
180 185 190
Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu Ile Asp
195 200 205
Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro Trp Gly
210 215 220
Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu Glu Glu
225 230 235 240
Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu Thr Asp
245 250 255

Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro Leu Lys
260 265 270
Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser Asp Gly
275 280 285
Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln Leu Val Phe
290 295 300
Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala Leu Val Arg
305 310 315 320
Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln Glu Ala Arg
325 330 335
Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val Ile Thr Gly
340 345 350
Ala Phe Lys Leu Val Thr Ala
355

<210> 100
<211> 578
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (277) ... (552)

<400> 100
cgccggggca ggtgttata ctccggaggg tggccccgtg cgtcatcggt ggagtggacc 60
aaaactggtg atctgttgc cctgtgtgac cttgcccaga accctgctga ctgagagaac 120
acatctgctg gaagtcctct gggattcaag gtacagggaa tgaagagtag ttttacagaa 180
aaaagaggac aatattggga tcaccccttga cctttccatt tgaaaataat attttctatt 240
gtgttataga aagggtggaa gctttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

caa agt ctt tta aca gct tagaaagtac agtagacata ctgggg 578
Gln Ser Leu Leu Thr Ala
90

<210> 101
<211> 92
<212> PRT
<213> Homo sapien

<400> 101
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
20 25 30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Leu Leu Thr Ala
85 90

<210> 102
<211> 768
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (277) ... (744)

<400> 102
cgccggggca ggtgtttata ctccggaggg tgtccccgtg cgtcatcggt ggagtggacc 60
aaaactggtg atctgtttgc cctgtgtgac cttgcccaga accctgctga ctgagagaac 120
acatctgctg gaagtcctct gggattcaag gtacaggaa tgaagagtag ttttacagaa 180
aaaagaggac aatattggga tcaccttga ctttccatt tggaaataat attttctatt 240
gtgttataga aaggtggaa gctttcatcc agaaca atg aat ttc ata aag gac 294
Met Asn Phe Ile Lys Asp
1 5

aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa 342
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln
10 15 20

atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta 390
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
25 30 35

aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc 438

Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
40 45 50

att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt 486
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
55 60 65 70

aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga 534
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly
75 80 85

caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct 582
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala
90 95 100

cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat 630
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr
105 110 115

ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc 678
Pro Leu Gly Glu Asp Ile Asp Ile Phe Asn Leu Lys Ser Thr Phe
120 125 130

aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag 726
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His Arg Val Glu
135 140 145 150

cag ctg acc cta gtt tta tagcatttc tacctgccccg ggcg 768
Gln Leu Thr Leu Val Leu
155

<210> 103
<211> 156
<212> PRT
<213> Homo sapien

<400> 103
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly
1 5 10 15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val
20 25 30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln
35 40 45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu
50 55 60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu
65 70 75 80
Phe Gln Asp Leu Asn Gly Gln Ser Leu Phe His Gln Thr Ser Glu Gly
85 90 95
Asp Leu Asp Asp Leu Ala Gln Asp Leu Lys Asp Leu Tyr His Thr Pro
100 105 110
Ser Phe Leu Asn Phe Tyr Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe

115	120	125
Asn Leu Lys Ser Thr Phe Thr Glu Pro Val Leu Trp Arg Lys Asp Gln		
130	135	140
His His His Arg Val Glu Gln Leu Thr Leu Val Leu		
145	150	155

<210> 104
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 104
aagaagagac ggctgcttat caat 24

<210> 105
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 105
ccacagcagg cctcgaagat gatc 24

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 106
atgatcctcc tgaagaagag 20

<210> 107
<211> 1009
<212> PRT
<213> Homo sapien

<400> 107
Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu
1 5 10 15
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu
20 25 30
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
35 40 45
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu

50	55	60
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala		
65	70	75
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly		80
85	90	95
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His		
100	105	110
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu		
115	120	125
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu		
130	135	140
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu		
145	150	155
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln		160
165	170	175
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala		
180	185	190
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln		
195	200	205
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu		
210	215	220
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met		
225	230	235
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Glu Leu		240
245	250	255
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val		
260	265	270
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His		
275	280	285
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe		
290	295	300
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val		
305	310	315
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu		320
325	330	335
Asp Ile Phe Gln Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr		
340	345	350
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg		
355	360	365
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn		
370	375	380
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser		
385	390	395
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu		400
405	410	415
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg		
420	425	430
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu		
435	440	445
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser		
450	455	460
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly		
465	470	475
		480

Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe
485 490 495
Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
500 505 510
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
515 520 525
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
530 535 540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545 550 555 560
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe
565 570 575
Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu
580 585 590
Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly
595 600 605
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile
610 615 620
Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625 630 635 640
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
645 650 655
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
660 665 670
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
675 680 685
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
690 695 700
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705 710 715 720
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
725 730 735
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
740 745 750
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
755 760 765
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
770 775 780
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn
785 790 795 800
Asn Ile Ser Asp Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His
805 810 815
Cys Glu Gln Leu Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala
820 825 830
Ala Gly Ala Gln Val Leu Ala Glu Gly Leu Arg Gly Asn Thr Ser Leu
835 840 845
Gln Phe Leu Gly Phe Trp Gly Asn Arg Val Gly Asp Glu Gly Ala Gln
850 855 860
Ala Leu Ala Glu Ala Leu Gly Asp His Gln Ser Leu Arg Trp Leu Ser
865 870 875 880
Leu Val Gly Asn Asn Ile Gly Ser Val Gly Ala Gln Ala Leu Ala Leu
885 890 895
Met Leu Ala Lys Asn Val Met Leu Glu Glu Leu Cys Leu Glu Asn

900	905	910
His Leu Gln Asp Glu Gly Val Cys Ser Leu Ala Glu Gly Leu Lys Lys		
915	920	925
Asn Ser Ser Leu Lys Ile Leu Asn Ile Lys Ile His Ala Ser Gly Phe		
930	935	940
Asn Lys Leu Leu Glu Ser Ile Phe Cys Ile Leu Leu Val Val Glu Ala		
945	950	955
Phe Phe Leu Gln Lys Val Val Lys Ile Leu Glu Glu Met Val Val Ser		
965	970	975
Trp Leu Glu Val Arg Leu Ser Asn Asn Cys Ile Thr Tyr Leu Gly Ala		
980	985	990
Glu Ala Leu Leu Gln Ala Leu Glu Arg Asn Asp Thr Ile Leu Glu Val		
995	1000	1005
Trp		

<210> 108

<400> 108
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<210> 109

<400> 109
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<210> 110

<400> 110
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<210> 111

<400> 111
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<210> 112

<220>
<221> VARIANT
<222> (1)...(87)
<223> Xaa = Any Amino Acid

<400> 112
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<210> 113

<400> 113
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<210> 114

<400> 114
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<210> 115

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<210> 143

<400> 143
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<210> 144

<400> 144
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<210> 145

<211> 30

<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 145
ccagaattca tggccgacaa ggtcctgaag 30

<210> 146
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 146
ccactcgagc taatttccag gtatcgacc 30

<210> 147
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 147
gaagacagtt acctggcaga 20

<210> 148
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 148
ttgtattctg aacatggcac c 21

<210> 149
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 149
gatcatcatc caggccgccc gtggtgacag ccctgg 36

<210> 150
<211> 36
<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 150

ccagggctgt caccacgggc ggctggatg atgatc

36

<210> 151

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 151

cggaattcat ggccgacaag gtccctg

26

<210> 152

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 152

cgctcgagtt agtcttgcattttaaggtaa tttccaga

38

<210> 153

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 153

catgtgaatg atccctctag cag

23

<210> 154

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 154

gggctcggct atcgtgctct a

21

<210> 155

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 155
acgatagccg agcccttatt c

21

<210> 156
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 156
gtatggaatg ttctgaatcg c

21

<210> 157
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 157
cccgatcca tgaatttcat aaaggacaat agc

33

<210> 158
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 158
ccttcgaac aagtccctgaa atagaggata

30

<210> 159
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 159
ggtggagcag gatgctgcta gagg

24

<210> 160
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 160
cacagtggtc caggctccga atgaagtca 29

<210> 161
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 161
catcatttgc tgcgagaagg tggag 25

<210> 162
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 162
ttaacttggta taacacttgg ctaag 25

<210> 163
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 163
gttaaacatca tttgctgcga gaa 23

<210> 164
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 164
ccggggcagg tagaagatgc tat 23

<210> 165
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 165
aatttcataa aggacaatag ccgag 25

<210> 166
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 166
tgtctactgt actttctaaag ctgtt 25

<210> 167
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (225)

<400> 167
gag agt act ccc tca gag atc ata gaa aga gaa aga aaa aag ttg ctt 48
Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu
1 5 10 15

gaa atc ctt caa cat gat cct gat tct atc tta gac acg tta act tct 96
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
20 25 30

cgg agg ctg att tct gag gaa gag tat gag act ctg gag aat gtt aca 144
Arg Arg Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
35 40 45

gat ctc ctg aag aaa agt cggt aag ctg tta att ttg gta cag aaa aag 192
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
50 55 60

gga gag gcg acc tgt cag cat ttt ctc aag tgt 225
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys

<210> 168
<211> 75
<212> PRT
<213> *Homo sapiens*

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<400> 168
Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys Lys Leu Leu
      1           5           10           15
Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
      20           25           30
Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
      35           40           45
Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
      50           55           60
Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys
      65           70           75

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<210> 169
<211> 228
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (1) ... (228)

<400> 169
atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg gtc gag 48
Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu
1 5 10 15

ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg gac tgg 96
 Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp
 20 25 30

ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc ttc cac 144
 Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
 35 40 45

ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg gac acc 192
 Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr
 50 55 60

gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc 228
 Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu
 65 70 75

<210> 170

<211> 76
<212> PRT
<213> Homo sapiens

<400> 170
Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu
1 5 10 15
Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp
20 25 30
Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
35 40 45
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr
50 55 60
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu
65 70 75

<210> 171
<211> 243
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (243)

<400> 171
cca gcc cga gac ctg cag agt cac cgg cca gcc att gtc agg agg ctc 48
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu
1 5 10 15
cac agc cat gtg gag aac atg ctg gac ctg gca tgg gag cgg ggt ttc 96
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe
20 25 30
gtc agc cag tat gaa tgt gat gaa atc agg ttg ccg atc ttc aca ccg 144
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro
35 40 45
tcc cag agg gca aga agg ctg ctt gat ctt gcc acg gtg aaa gcg aat 192
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn
50 55 60
gga ttg gct gcc ttc ctt cta caa cat gtt cag gaa tta cca gtc cca 240
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro
65 70 75 80
ttg
Leu 243

<210> 172

<211> 81
<212> PRT
<213> Homo sapiens

<400> 172
Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu
1 5 10 15
His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe
20 25 30
Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro
35 40 45
Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn
50 55 60
Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro
65 70 75 80
Leu

<210> 173
<211> 888
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (888)

<400> 173
gac gat gcg gac act gtg ctg gtg ggt gag gcg ggc agt ggc aag 48
Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys
1 5 10 15
agc acg ctc ctg cag cgg ctg cac ttg ctg tgg gct gca ggg caa gac 96
Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp
20 25 30
ttc cag gaa ttt ctc ttt gtc ttc cca ttc agc tgc cgg cag ctg cag 144
Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln
35 40 45
tgc atg gcc aaa cca ctc tct gtg cgg act cta ctc ttt gag cac tgc 192
Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys
50 55 60
tgt tgg cct gat gtt ggt caa gaa gac atc ttc cag tta ctc ctt gag 240
Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Asp
65 70 75 80
cac cct gac cgt gtc ctg tta acc ttt gat ggc ttt gac gag ttc aag 288
His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys
85 90 95

ttc agg ttc acg gat cgt gaa cgc cac tgc tcc ccg acc gac ccc acc		336
Phe Arg Phe Thr Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr		
100	105	110
tct gtc cag acc ctg ctc ttc aac ctt ctg cag ggc aac ctg ctg aag		384
Ser Val Gln Thr Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys		
115	120	125
aat gcc cgc aag gtg gtg acc agc cgt ccg gcc gct gtg tcg gcg ttc		432
Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe		
130	135	140
ctc agg aag tac atc cgc acc gag ttc aac ctc aag ggc ttc tct gaa		480
Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu		
145	150	155
160		
cag ggc atc gag ctg tac ctg agg aag cgc cat cat gag ccc ggg gtg		528
Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val		
165	170	175
gcg gac cgc ctc atc cgc ctg ctc caa gag acc tca gcc ctg cac ggt		576
Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly		
180	185	190
ttg tgc cac ctg cct gtc ttc tca tgg atg gtg tcc aaa tgc cac cag		624
Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln		
195	200	205
gaa ctg ttg ctg cag gag ggg ggg tcc cca aag acc act aca gat atg		672
Glu Leu Leu Leu Gln Glu Gly Ser Pro Lys Thr Thr Asp Met		
210	215	220
tac ctg ctg att ctg cag cat ttt ctg ctg cat gcc acc ccc cca gac		720
Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp		
225	230	235
240		
tca gct tcc caa ggt ctg gga ccc agt ctt ctt cgg ggc cgc ctc ccc		768
Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro		
245	250	255
acc ctc ctg cac ctg ggc aga ctg gct ctg tgg ggc ctg ggc atg tgc		816
Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys		
260	265	270
tgc tac gtg ttc tca gcc cag cag ctc cag gca gca cag gtc agc cct		864
Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro		
275	280	285
gat gac att tct ctt ggc ttc ctg		888
Asp Asp Ile Ser Leu Gly Phe Leu		
290	295	

<210> 174
<211> 296
<212> PRT
<213> Homo sapiens

<400> 174
Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys
1 5 10 15
Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp
20 25 30
Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln
35 40 45
Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys
50 55 60
Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Leu Asp
65 70 75 80
His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys
85 90 95
Phe Arg Phe Thr Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr
100 105 110
Ser Val Gln Thr Leu Leu Phe Asn Leu Leu Gln Gly Asn Leu Leu Lys
115 120 125
Asn Ala Arg Lys Val Val Thr Ser Arg Pro Ala Ala Val Ser Ala Phe
130 135 140
Leu Arg Lys Tyr Ile Arg Thr Glu Phe Asn Leu Lys Gly Phe Ser Glu
145 150 155 160
Gln Gly Ile Glu Leu Tyr Leu Arg Lys Arg His His Glu Pro Gly Val
165 170 175
Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser Ala Leu His Gly
180 185 190
Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser Lys Cys His Gln
195 200 205
Glu Leu Leu Leu Gln Glu Gly Ser Pro Lys Thr Thr Thr Asp Met
210 215 220
Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala Thr Pro Pro Asp
225 230 235 240
Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg Gly Arg Leu Pro
245 250 255
Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly Leu Gly Met Cys
260 265 270
Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala Gln Val Ser Pro
275 280 285
Asp Asp Ile Ser Leu Gly Phe Leu
290 295

<210> 175
<211> 1209
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (1) . . . (1209)

<400> 175
 gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc caa gag acc tca 48
 Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser
 1 5 10 15

 gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca tgg atg gtg tcc 96
 Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser
 20 25 30

 aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg tcc cca aag acc 144
 Lys Cys His Gln Glu Leu Leu Leu Gln Glu Gly Ser Pro Lys Thr
 35 40 45

 act aca gat atg tac ctg ctg att ctg cag cat ttt ctg ctg cat gcc 192
 Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala
 50 55 60

 acc ccc cca gac tca gct tcc caa ggt ctg gga ccc agt ctt ctt cgg 240
 Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg
 65 70 75 80

 ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg gct ctg tgg ggc 288
 Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly
 85 90 95

 ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag ctc cag gca gca 336
 Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala
 100 105 110

 cag gtc agc cct gat gac att tct ctt ggc ttc ctg gtg cgt gcc aaa 384
 Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg Ala Lys
 115 120 125

 ggt gtc gtg cca ggg agt acg gcg ccc ctg gaa ttc ctt cac atc act 432
 Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His Ile Thr
 130 135 140

 ttc cag tgc ttc ttt gcc gcg ttc tac ctg gca ctc agt gct gat gtg 480
 Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala Asp Val
 145 150 155 160

 cca cca gct ttg ctc aga cac ctc ttc aat tgt ggc agg cca ggc aac 528
 Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro Gly Asn
 165 170 175

 tca cca atg gcc agg ctc ctg ccc acg atg tgc atc cag gcc tcg gag 576
 Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala Ser Glu
 180 185 190

 gga aag gac agc agc gtg gca gct ttg ctg cag aag gcc gag ccg cac 624
 Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu Pro His

195

200

205

aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg ttg tcc cg	gag	672
Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser Arg Glu		
210	215	220
cac tgg ggc ctg ctg gct gag tgc cag aca tct gag aag gcc ctg ctc		720
His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala Leu Leu		
225	230	235
240		
cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc agc ctc cgc aag		768
Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu Arg Lys		
245	250	255
cac ttc cac tcc atc ccg cca gct gca ccg ggt gag gcc aag agc gtg		816
His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys Ser Val		
260	265	270
cat gcc atg ccc ggg ttc atc tgg ctc atc ccg agc ctg tac gag atg		864
His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met		
275	280	285
cag gag gag cgg ctg gct cgg aag gct gca cgt ggc ctg aat gtt ggg		912
Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn Val Gly		
290	295	300
cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act gag tgt gct gcc		960
His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys Ala Ala		
305	310	315
320		
ctg gcc ttt gtg ctg cag cac ctc ccg ccc gtg gcc ctg cag ctg		1008
Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu Gln Leu		
325	330	335
gac tac aac tct gtg ggt gac att ggc gtg gag cag ctg ctg cct tgc		1056
Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu Pro Cys		
340	345	350
ctt ggt gtc tgc aag gct ctg tat ttg cgc gat aac aat atc tca gac		1104
Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile Ser Asp		
355	360	365
cga ggc atc tgc aag ctc att gaa tgt gct ctt cac tgc gag caa ttg		1152
Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu		
370	375	380
cag aag tta gcg ctg ggg aat aac tac atc act gcc gcg gga gcc caa		1200
Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln		
385	390	395
400		
gtg ctg gcc		1209
Val Leu Ala		

<210> 176
<211> 403
<212> PRT
<213> Homo sapiens

<400> 176
Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu Gln Glu Thr Ser
1 5 10 15
Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser Trp Met Val Ser
20 25 30
Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly Ser Pro Lys Thr
35 40 45
Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe Leu Leu His Ala
50 55 60
Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro Ser Leu Leu Arg
65 70 75 80
Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu Ala Leu Trp Gly
85 90 95
Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln Leu Gln Ala Ala
100 105 110
Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu Val Arg Ala Lys
115 120 125
Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe Leu His Ile Thr
130 135 140
Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu Ser Ala Asp Val
145 150 155 160
Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly Arg Pro Gly Asn
165 170 175
Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile Gln Ala Ser Glu
180 185 190
Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys Ala Glu Pro His
195 200 205
Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu Leu Ser Arg Glu
210 215 220
His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu Lys Ala Leu Leu
225 230 235 240
Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg Ser Leu Arg Lys
245 250 255
His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu Ala Lys Ser Val
260 265 270
His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met
275 280 285
Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly Leu Asn Val Gly
290 295 300
His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr Glu Cys Ala Ala
305 310 315 320
Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val Ala Leu Gln Leu
325 330 335
Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln Leu Leu Pro Cys
340 345 350
Leu Gly Val Cys Lys Ala Leu Tyr Leu Arg Asp Asn Asn Ile Ser Asp

355	360	365
Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu		
370	375	380
Gln Lys Leu Ala Leu Gly Asn Asn Tyr Ile Thr Ala Ala Gly Ala Gln		
385	390	395
Val Leu Ala		400

<210> 177
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (261)

<400> 177			
atg aat ttc ata aag gac aat agc cga gcc ctt att caa aga atg gga			48
Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly			
1	5	10	15
atg act gtt ata aag caa atc aca gat gac cta ttt gta tgg aat gtt			96
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val			
20	25	30	
ctg aat cgc gaa gaa gta aac atc att tgc tgc gag aag gtg gag cag			144
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln			
35	40	45	
gat gct gct aga ggg atc att cac atg att ttg aaa aag ggt tca gag			192
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu			
50	55	60	
tcc tgt aac ctc ttt ctt aaa tcc ctt aag gag tgg aac tat cct cta			240
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu			
65	70	75	80
ttt cag gac ttg aat gga caa			261
Phe Gln Asp Leu Asn Gly Gln			
85			

<210> 178
<211> 87
<212> PRT
<213> Homo sapiens

<400> 178

Met Asn Phe Ile Lys Asp Asn Ser Arg Ala Leu Ile Gln Arg Met Gly			
1	5	10	15
Met Thr Val Ile Lys Gln Ile Thr Asp Asp Leu Phe Val Trp Asn Val			

20	25	30
Leu Asn Arg Glu Glu Val Asn Ile Ile Cys Cys Glu Lys Val Glu Gln		
35	40	45
Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu		
50	55	60
Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu		
65	70	75
Phe Gln Asp Leu Asn Gly Gln		
	85	

<210> 179

<211> 891

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(891)

<400> 179		
cct cag agc ccc tgc atc att gaa ggg gaa tct ggc aaa ggc aag tcc		48
Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser		
1	5	10
		15
act ctg ctg cag cgc att gcc atg ctc tgg ggc tcc gga aag tgc aag		96
Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys		
20	25	30
gct ctg acc aag ttc aaa ttc gtc ttc ctc cgt ctc agc agg gcc		144
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala		
35	40	45
cag ggt gga ctt ttt gaa acc ctc tgt gat caa ctc ctg gat ata cct		192
Gln Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro		
50	55	60
ggc aca atc agg aag cag aca ttc atg gcc atg ctg ctg aag ctg cgg		240
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg		
65	70	75
		80
cag agg gtt ctt ttc ctt ctt gat ggc tac aat gaa ttc aag ccc cag		288
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln		
85	90	95
aac tgc cca gaa atc gaa gcc ctg ata aag gaa aac cac cgc ttc aag		336
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys		
100	105	110
aac atg gtc atc gtc acc act acc act gag tgc ctg agg cac ata cgg		384
Asn Met Val Ile Val Thr Thr Glu Cys Leu Arg His Ile Arg		
115	120	125

cag ttt ggt gcc ctg act gct gag gtg ggg gat atg aca gaa gac agc Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser	432
130 135 140	
gcc cag gct ctc atc cga gaa gtg ctg atc aag gag ctt gct gaa ggc Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly	480
145 150 155 160	
ttg ttg ctc caa att cag aaa tcc agg tgc ttg agg aat ctc atg aag Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys	528
165 170 175	
acc cct ctc ttt gtg gtc atc act tgt gca atc cag atg ggt gaa agt Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser	576
180 185 190	
gag ttc cac tct cac aca caa aca acg ctg ttc cat acc ttc tat gat Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp	624
195 200 205	
ctg ttg ata cag aaa aac aaa cac aaa cat aaa ggt gtg gct gca agt Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser	672
210 215 220	
gac ttc att cgg agc ctg gac cac cgt gga gac cta gct ctg gag ggt Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly	720
225 230 235 240	
gtg ttc tcc cac aag ttt gat ttc gaa ctg cag gat gtg tcc agc gtg Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val	768
245 250 255	
aat qag gat gtc ctg ctg aca act ggg ctc ctc tgt aaa tat aca gct Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala	816
260 265 270	
caa agg ttc aag cca aag tat aaa ttc ttt cac aag tca ttc cag gag Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu	864
275 280 285	
tac aca gca gga cga aga ctc agc agt Tyr Thr Ala Gly Arg Arg Leu Ser Ser	891
290 295	

<210> 180
<211> 297
<212> PRT
<213> Homo sapiens

<400> 180
Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser
1 5 10 15

Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys
20 25 30
Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala
35 40 45
Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
50 55 60
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
65 70 75 80
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
85 90 95
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys
100 105 110
Asn Met Val Ile Val Thr Thr Glu Cys Leu Arg His Ile Arg
115 120 125
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
130 135 140
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
145 150 155 160
Leu Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
165 170 175
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
180 185 190
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
195 200 205
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
210 215 220
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
225 230 235 240
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
245 250 255
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
260 265 270
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
275 280 285
Tyr Thr Ala Gly Arg Arg Leu Ser Ser
290 295

<210> 181

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (618)

<400> 181

gg t a a c t t g a a g a a c c t t a c a a a g c t c a t a a t g g a t a a c a t a a a g a t g 48
Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
1 5 10 15

a a t g a a a g a t g c t a a a c t a g c t g a a a c t g a a g 96

Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys			
20	25	30	
aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag gga			144
Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly			
35	40	45	
atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt gaa			192
Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu			
50	55	60	
gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa atc			240
Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile			
65	70	75	80
cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat tta			288
Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu			
85	90	95	
tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa ctg			336
Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu			
100	105	110	
atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg ccc			384
Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro			
115	120	125	
tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat ttg			432
Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu			
130	135	140	
gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga ctc			480
Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu			
145	150	155	160
aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac cct			528
Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro			
165	170	175	
ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc agt			576
Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser			
180	185	190	
gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag			618
Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys			
195	200	205	

<210> 182
<211> 206
<212> PRT
<213> Homo sapiens

<400> 182

Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
1 5 10 15
Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys
20 25 30
Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly
35 40 45
Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu
50 55 60
Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile
65 70 75 80
Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu
85 90 95
Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu
100 105 110
Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro
115 120 125
Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu
130 135 140
Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu
145 150 155 160
Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro
165 170 175
Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser
180 185 190
Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys
195 200 205

<210> 183

<211> 165

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(165)

<400> 183

acc tac att ccc agc agg gct gta tct ttg ttc aac tgg aag cag 48
Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln
1 5 10 15

gaa ttc agg act ctg gag gtc aca ctc cggtt ttc agc aag ttg aat 96
Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn
20 25 30

aag caa gat atc aga tat ctg ggg aaa ata ttc agc tct gcc aca agc 144
Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser
35 40 45

ctc agg ctg caa ata aag aga 165

Leu Arg Leu Gln Ile Lys Arg
50 55

<210> 184
<211> 55
<212> PRT
<213> Homo sapiens

<400> 184
Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln
1 5 10 15
Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn
20 25 30
Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser
35 40 45
Leu Arg Leu Gln Ile Lys Arg
50 55

<210> 185
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 185
gaaatgtgct cgcaggagg 19

<210> 186
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 186
gatgagcttc tgacaggccc 20

<210> 187
<211> 3063
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (2385)

<221> CDS
<222> (2389) ... (2928)

<400> 187
 tgt gaa atg tgc tcg cag gag gct ttt cag gca cag agg agc cag ctg 48
 Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu
 1 5 10 15

 gtc gag ctg ctg gtc tca ggg tcc ctg gaa ggc ttc gag agt gtc ctg 96
 Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu
 20 25 30

 gac tgg ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc 144
 Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
 35 40 45

 ttc cac ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg 192
 Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu
 50 55 60

 gac acc gtc tgg aat aag ggt act tgg gcc tgg cag aag ctc atc gcg 240
 Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala
 65 70 75 80

 gct gcc caa gaa gcc cag gcc gac agc cag tcc ccc aag ctg cat ggc 288
 Ala Ala Gln Glu Ala Gln Asp Ser Gln Ser Pro Lys Leu His Gly
 85 90 95

 tgc tgg gac ccc cac tgc ctc cac cca gcc cga gac ctg cag agt cac 336
 Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His
 100 105 110

 cgg cca gcc att gtc agg agg ctc cac agc cat gtg gag aac atg ctg 384
 Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu
 115 120 125

 gac ctg gca tgg gag cggt ttc gtc agc cag tat gaa tgt gat gaa 432
 Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu
 130 135 140

 atc agg ttg ccg atc ttc aca ccg tcc cag agg gca aga agg ctg ctt 480
 Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu
 145 150 155 160

 gat ctt gcc acg gtg aaa gcg aat gga ttg gct gcc ttc ctt cta caa 528
 Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln
 165 170 175

 cat gtt cag gaa tta cca gtc cca ttg gcc ctg cct ttg gaa gct gcc 576
 His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala
 180 185 190

 aca tgc aag aag tat atg gcc aag ctg agg acc acg gtg tct gct cag 624
 Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln
 195 200 205

tct cgc ttc ctc agt acc tat gat gga gca gag acg ctc tgc ctg gag 672
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu
210 215 220

gac ata tac aca gag aat gtc ctg gag gtc tgg gca gat gtg ggc atg 720
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met
225 230 235 240

gct gga ccc ccg cag aag agc cca gcc acc ctg ggc ctg gag gag ctc 768
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Leu
245 250 255

ttc agc acc cct ggc cac ctc aat gac gat gcg gac act gtg ctg gtg 816
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val
260 265 270

gtg ggt gag gcg ggc agt ggc aag agc acg ctc ctg cag cgg ctg cac 864
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His
275 280 285

ttg ctg tgg gct gca ggg caa gac ttc cag gaa ttt ctc ttt gtc ttc 912
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe
290 295 300

cca ttc agc tgc cgg cag ctg cag tgc atg gcc aaa cca ctc tct gtg 960
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val
305 310 315 320

cgg act cta ctc ttt gag cac tgc tgt tgg cct gat gtt ggt caa gaa 1008
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu
325 330 335

gac atc ttc cag tta ctc ctt gac cac cct gac cgt gtc ctg tta acc 1056
Asp Ile Phe Gln Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr
340 345 350

ttt gat ggc ttt gac gag ttc aag ttc agg ttc acg gat cgt gaa cgc 1104
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg
355 360 365

cac tgc tcc ccg acc gac ccc acc tct gtc cag acc ctg ctc ttc aac 1152
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn
370 375 380

ctt ctg cag ggc aac ctg ctg aag aat gcc cgc aag gtg gtg acc agc 1200
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser
385 390 395 400

cgt ccg gcc gct gtg tcg gcg ttc ctc agg aag tac atc cgc acc gag 1248
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu
405 410 415

ttc aac ctc aag ggc ttc tct gaa cag ggc atc gag ctg tac ctg agg Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg 420 425 430	1296
aag cgc cat cat gag ccc ggg gtg gcg gac cgc ctc atc cgc ctg ctc Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu 435 440 445	1344
caa gag acc tca gcc ctg cac ggt ttg tgc cac ctg cct gtc ttc tca Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser 450 455 460	1392
tgg atg gtg tcc aaa tgc cac cag gaa ctg ttg ctg cag gag ggg ggg Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly 465 470 475 480	1440
tcc cca aag acc act aca gat atg tac ctg ctg att ctg cag cat ttt Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe 485 490 495	1488
ctg ctg cat gcc acc ccc cca gac tca gct tcc caa ggt ctg gga ccc Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro 500 505 510	1536
agt ctt ctt cgg ggc cgc ctc ccc acc ctc ctg cac ctg ggc aga ctg Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu 515 520 525	1584
gct ctg tgg ggc ctg ggc atg tgc tgc tac gtg ttc tca gcc cag cag Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln 530 535 540	1632
ctc cag gca gca cag gtc agc cct gat gac att tct ctt ggc ttc ctg Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu 545 550 555 560	1680
gtg cgt gcc aaa ggt gtc gtg cca ggg agt acg gcg ccc ctg gaa ttc Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe 565 570 575	1728
ctt cac atc act ttc cag tgc ttc ttt gcc gcg ttc tac ctg gca ctc Leu His Ile Thr Phe Gln Cys Phe Ala Ala Phe Tyr Leu Ala Leu 580 585 590	1776
agt gct gat gtg cca cca gct ttg ctc aga cac ctc ttc aat tgt ggc Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly 595 600 605	1824
agg cca ggc aac tca cca atg gcc agg ctc ctg ccc acg atg tgc atc Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile 610 615 620	1872
cag gcc tcg gag gga aag gac agc agc gtg gca gct ttg ctg cag aag	1920

Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625 630 635 640

gcc gag ccg cac aac ctt cag atc aca gca gcc ttc ctg gca ggg ctg 1968
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
645 650 655

ttg tcc cgg gag cac tgg ggc ctg ctg gct gag tgc cag aca tct gag 2016
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
660 665 670

aag gcc ctg ctc cgg cgc cag gcc tgt gcc cgc tgg tgt ctg gcc cgc 2064
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
675 680 685

agc ctc cgc aag cac ttc cac tcc atc ccg cca gct gca ccg ggt gag 2112
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
690 695 700

gcc aag agc gtg cat gcc atg ccc ggg ttc atc tgg ctc atc ccg agc 2160
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705 710 715 720

ctg tac gag atg cag gag gag cgg ctg gct cgg aag gct gca cgt ggc 2208
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
725 730 735

ctg aat gtt ggg cac ctc aag ttg aca ttt tgc agt gtg ggc ccc act 2256
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
740 745 750

gag tgt gct gcc ctg gcc ttt gtg ctg cag cac ctc ccg cgg ccc gtg 2304
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
755 760 765

gcc ctg cag ctg gac tac aac tct gtg ggt gac att ggc gtg gag cag 2352
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
770 775 780

ctg ctg cct tgc ctt ggt gtc tgc aag gct ctg taa ttc tgg ggc aac 2400
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu Phe Trp Gly Asn
785 790 795

aga gtg ggt gac gag ggg gcc cag gcc ctg gct gaa gcc ttg ggt gat 2448
Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu Ala Leu Gly Asp
800 805 810 815

cac cag agc ttg agg tgg ctc agc ctg gtg ggg aac aac att ggc agt 2496
His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn Asn Ile Gly Ser
820 825 830

gtg ggt gcc caa gcc ttg gca ctg atg ctg gca aag aac gtc atg cta 2544
Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys Asn Val Met Leu

835

840

845

gaa gaa ctc tgc ctg gag gag aac cat ctc cag gat gaa ggt gta tgt 2592
Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp Glu Gly Val Cys
850 855 860

tct ctc gca gaa gga ctg aag aaa aat tca agt ttg aaa atc ctg aac 2640
Ser Leu Ala Glu Gly Leu Lys Lys Asn Ser Ser Leu Lys Ile Leu Asn
865 870 875

ata aaa att cat gct tcg gga ttc aac aaa ctc ttg gaa agc att ttc 2688
Ile Lys Ile His Ala Ser Gly Phe Asn Lys Leu Leu Glu Ser Ile Phe
880 885 890 895

tgc atc ctc ctg gtt gtg gaa gca ttt ttc ctg cag aaa gtt gtc aag 2736
Cys Ile Leu Leu Val Val Glu Ala Phe Phe Leu Gln Lys Val Val Lys
900 905 910

att ctt gaa gaa atg gta gtc agt tgg cta gag gtc agg ttg tcc aat 2784
Ile Leu Glu Met Val Val Ser Trp Leu Glu Val Arg Leu Ser Asn
915 920 925

aac tgc atc acc tac cta ggg gca gaa gcc ctc ctg cag gcc ctt gaa 2832
Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu Leu Gln Ala Leu Glu
930 935 940

agg aat gac acc atc ctg gaa gtc tgg ctc cga ggg aac act ttc tct 2880
Arg Asn Asp Thr Ile Leu Glu Val Trp Leu Arg Gly Asn Thr Phe Ser
945 950 955

cta gag gag gtt gac aag ctc ggc tgc agg gac acc aga ctc ttg ctt 2928
Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp Thr Arg Leu Leu Leu
960 965 970 975

tgaagtctcc gggaggatgt tcgtctcagt ttgttgtga gcaggctgtg agtttgggcc 2988
ccagaggctg ggtgacatgt gttggcagcc tcttcaaaat gagccctgtc ctgcctaagg 3048
ctgaacttgt tttct 3063

<210> 188

<211> 795

<212> PRT

<213> Homo sapiens

<400> 188
Cys Glu Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu
1 5 10 15
Val Glu Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu
20 25 30
Asp Trp Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly
35 40 45
Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu
50 55 60
Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala

65	70	75	80
Ala Ala Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly			
85	90	95	
Cys Trp Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His			
100	105	110	
Arg Pro Ala Ile Val Arg Arg Leu His Ser His Val Glu Asn Met Leu			
115	120	125	
Asp Leu Ala Trp Glu Arg Gly Phe Val Ser Gln Tyr Glu Cys Asp Glu			
130	135	140	
Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Arg Leu Leu			
145	150	155	160
Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln			
165	170	175	
His Val Gln Glu Leu Pro Val Pro Leu Ala Leu Pro Leu Glu Ala Ala			
180	185	190	
Thr Cys Lys Lys Tyr Met Ala Lys Leu Arg Thr Thr Val Ser Ala Gln			
195	200	205	
Ser Arg Phe Leu Ser Thr Tyr Asp Gly Ala Glu Thr Leu Cys Leu Glu			
210	215	220	
Asp Ile Tyr Thr Glu Asn Val Leu Glu Val Trp Ala Asp Val Gly Met			
225	230	235	240
Ala Gly Pro Pro Gln Lys Ser Pro Ala Thr Leu Gly Leu Glu Leu			
245	250	255	
Phe Ser Thr Pro Gly His Leu Asn Asp Asp Ala Asp Thr Val Leu Val			
260	265	270	
Val Gly Glu Ala Gly Ser Gly Lys Ser Thr Leu Leu Gln Arg Leu His			
275	280	285	
Leu Leu Trp Ala Ala Gly Gln Asp Phe Gln Glu Phe Leu Phe Val Phe			
290	295	300	
Pro Phe Ser Cys Arg Gln Leu Gln Cys Met Ala Lys Pro Leu Ser Val			
305	310	315	320
Arg Thr Leu Leu Phe Glu His Cys Cys Trp Pro Asp Val Gly Gln Glu			
325	330	335	
Asp Ile Phe Gln Leu Leu Asp His Pro Asp Arg Val Leu Leu Thr			
340	345	350	
Phe Asp Gly Phe Asp Glu Phe Lys Phe Arg Phe Thr Asp Arg Glu Arg			
355	360	365	
His Cys Ser Pro Thr Asp Pro Thr Ser Val Gln Thr Leu Leu Phe Asn			
370	375	380	
Leu Leu Gln Gly Asn Leu Leu Lys Asn Ala Arg Lys Val Val Thr Ser			
385	390	395	400
Arg Pro Ala Ala Val Ser Ala Phe Leu Arg Lys Tyr Ile Arg Thr Glu			
405	410	415	
Phe Asn Leu Lys Gly Phe Ser Glu Gln Gly Ile Glu Leu Tyr Leu Arg			
420	425	430	
Lys Arg His His Glu Pro Gly Val Ala Asp Arg Leu Ile Arg Leu Leu			
435	440	445	
Gln Glu Thr Ser Ala Leu His Gly Leu Cys His Leu Pro Val Phe Ser			
450	455	460	
Trp Met Val Ser Lys Cys His Gln Glu Leu Leu Gln Glu Gly Gly			
465	470	475	480
Ser Pro Lys Thr Thr Asp Met Tyr Leu Leu Ile Leu Gln His Phe			
485	490	495	

Leu Leu His Ala Thr Pro Pro Asp Ser Ala Ser Gln Gly Leu Gly Pro
500 505 510
Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu
515 520 525
Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln
530 535 540
Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu
545 550 555 560
Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe
565 570 575
Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu
580 585 590
Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly
595 600 605
Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile
610 615 620
Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys
625 630 635 640
Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu
645 650 655
Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu
660 665 670
Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg
675 680 685
Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu
690 695 700
Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser
705 710 715 720
Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly
725 730 735
Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr
740 745 750
Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val
755 760 765
Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln
770 775 780
Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu
785 790 795

<210> 189
<211> 180
<212> PRT
<213> Homo sapiens

<400> 189
Phe Trp Gly Asn Arg Val Gly Asp Glu Gly Ala Gln Ala Leu Ala Glu
1 5 10 15
Ala Leu Gly Asp His Gln Ser Leu Arg Trp Leu Ser Leu Val Gly Asn
20 25 30
Asn Ile Gly Ser Val Gly Ala Gln Ala Leu Ala Leu Met Leu Ala Lys
35 40 45
Asn Val Met Leu Glu Glu Leu Cys Leu Glu Glu Asn His Leu Gln Asp

<210> 190
<211> 721
<212> DNA
<213> *Mus musculus*

<220>
<221> CDS
<222> (193) . . . (612)

<400> 190
 cctggggttc ctgcacatta ccttcgtgc tttttgcgg ctttctactt ggctgtcagt 60
 gctgacacat cggtggcctc tctcaagcac ctttcagct gtggccggct gggcagctca 120
 ctgctggaa ggctgctgcc caacctgtgt atccagggct ccagagtcaa gaagggcagc 180
 gaagcagccc tg ctg cag aag gag cca cac aac ctg caa atc aca gca 231
 Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala
 1 5 10

```

gcc ttc cta gca ggt ctg ttg tcc cag cag cat cggt gac ctg ttg gct 279
Ala Phe Leu Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala
15          20          25

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gca tgc cag gtc tcc gag agg gta ctg ctc cag cgt cag gca cgt gcc 327
Ala Cys Gln Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala
 30           35           40           45

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cgc tcg tgt ctg gcc cac agc ctc cgc gag cac ttc cat tcc atc ccg 375
 Arg Ser Cys Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro
 50 55 60

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cct gcc gtg ccc ggt gag acc aag agc atg cat gct atg ccg ggc ttc 423
Pro Ala Val Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe
65          70          75

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att tgg ctc atc cgt agc ctg tac gaa atg cag gag gag gag cag ttg gcc 471

Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala
80 85 90

cag gag gct gtc cgt cgc ttg gac atc ggg cac ctg aag ttg aca ttt 519
Gln Glu Ala Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe
95 100 105

tgc aga gtg ggc cct gca gag tgt gct gca ctg gcc ttt gta ctg caa 567
Cys Arg Val Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln
110 115 120 125

cat ctc cag cgg cct gtg gcc cta cag ctg gat tac aac tct gtg 612
His Leu Gln Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val
130 135 140

ggagatgttg ggagtggAAC agctgcgacc gtgccttgg ggtctgcaca gctctgttagt 672
gagtgtgaca aggtcttgCC gattgggcCT gtggcaaATg ctactgtca 721

<210> 191

<211> 140

<212> PRT

<213> Mus musculus

<400> 191

Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu
1 5 10 15
Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala Ala Cys Gln
20 25 30
Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
35 40 45
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
50 55 60
Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu
65 70 75 80
Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala
85 90 95
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val
100 105 110
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln
115 120 125
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser Val
130 135 140

<210> 192

<211> 419

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1) ... (417)

<400> 192

ctg cag aag gct gag cca cac aac ctg cag atc aca gca gcc ttc cta 48
Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu
1 5 10 15

gca ggt ctg ttg tcc cag cag cat cgg gac ctg ttg gct gca tgc cag 96
Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala Ala Cys Gln
20 25 30

atc tcc gag agg gtg ctg ctc cag cgt cag gca cgt gcc cgc tcg tgt 144
Ile Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
35 40 45

ctg gcc cac agc ctc cgc gag cac ttc cat tcc atc ccg cct gcc gtg 192
Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
50 55 60

ccc ggt gag acc aag agc atg cat gct atg ccg ggc ttt att tgg ctc 240
Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu
65 70 75 80

atc cgg agc ctg tac gag atg cag gag cag ttg gcc cag gag gct 288
Ile Arg Ser Leu Tyr Glu Met Gln Glu Gln Leu Ala Gln Glu Ala
85 90 95

gtc cgt cgc ttg gac atc ggg cac ctg aag ttg aca ttt tgc aga gtg 336
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val
100 105 110

ggc cct gca gag tgt gct gcg ctg gcc ttt gta ctg caa cat ctc cag 384
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln
115 120 125

cgg cct gtg gcc cta cag ctg gat tac aac tct gt 419
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser
130 135

<210> 193

<211> 139

<212> PRT

<213> Mus musculus

<400> 193

Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu
1 5 10 15

Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala Ala Cys Gln
20 25 30

Ile Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala Arg Ser Cys
35 40 45

Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro Pro Ala Val
50 55 60

Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe Ile Trp Leu

65	70	75	80
Ile Arg Ser Leu Tyr Glu Met Gln Glu Glu Gln Leu Ala Gln Glu Ala			
85	90	95	
Val Arg Arg Leu Asp Ile Gly His Leu Lys Leu Thr Phe Cys Arg Val			
100	105	110	
Gly Pro Ala Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Gln			
115	120	125	
Arg Pro Val Ala Leu Gln Leu Asp Tyr Asn Ser			
130	135		

<210> 194

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 194

ctgcagaagg ctgagccaca caacct

26

<210> 195

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 195

acagagttgt aatccagctg tagggccaca

30